Amendments to the Claims:

The following listing of claims replaces all prior versions of the claims:

Listing of Claims:

1. (previously presented) A method of identifying one or more positions in a <u>protein</u> ~~polymer~~ family, the method comprising:
   (a) accessing data representing a multiple sequence alignment (MSA) of a plurality of <u>protein</u> ~~polymer~~ sequences; and
   (b) identifying one or more evolutionarily conserved amino acid positions within the MSA using the following equation:

$$\Delta G_i^{stat} = kT^* \sqrt{\sum_x \left(\ln \frac{P_i^x}{P_{MSA}^x} \right)^2}$$

   wherein:

   i is a position in the MSA;

   ΔG_i^{stat} is the conservation energy value for position i;

   P_i^x is the probability of <u>amino acid</u> ~~monomer~~ x at position i;

   P_{MSA}^x is the probability of <u>amino acid</u> ~~monomer~~ x in the MSA; and

   kT* is an energy unit, where k is Boltzmann's constant.

2. (original) The method of claim 1, wherein the method is executed using a machine.

3. (previously presented) A program storage device comprising machine readable instructions for performing the operations recited in claim 1.

4. (previously presented) The method of claim 1, further comprising generating a graphical image of one or more conservation energy values calculated using the equation.

5-6. (canceled)

7.   (previously presented) The method of claim 1, wherein the data accessed comprises data from the PSD-95 (Postsynaptic density protein of Mr 95kDa), Dlg (Drosophila Discs-Large protein) and ZO-1 (Zonula occludens protein 1) protein family.

8.   (previously presented) The method of claim 1, wherein the data accessed comprises data from the p21^{ras} protein family.

9.   (previously presented) The method of claim 1, wherein the data accessed comprises data from the hemoglobin protein family.

10.   (currently amended) A method of identifying one or more positions in a <u>protein</u> ~~polymer~~ family, the method comprising:

(a)   accessing data representing a multiple sequence alignment (MSA) of a plurality of <u>protein</u> ~~polymer~~ sequences;

(b)   calculating a conservation energy value for each position in the MSA using the following equation:

$$\Delta G_i^{stat} = kT^* \sqrt{\sum_x \left(\ln \frac{P_i^x}{P_{MSA}^x} \right)^2}$$

wherein:

i is a position in the MSA;

ΔG_i^{stat} is the conservation energy value for position i;

P_i^x is the probability of <u>amino acid</u> ~~monomer~~ x at position i;

P_{MSA}^x is the probability of <u>amino acid</u> ~~monomer~~ x in the MSA;

kT* is an energy unit, where k is Boltzmann's constant; and

(c)   identifying one or more positions within the MSA that have statistically significant conservation energy values.

11.   (original) The method of claim 10, wherein the method is executed using a machine.

12.   (previously presented) A program storage device comprising machine readable instructions for performing the operations recited in claim 10.

13.   (original) The method of claim 10, further comprising generating a graphical image of the conservation energy values.

14-15. (canceled)

16.   (previously presented) The method of claim 10, wherein the data accessed comprises data from the PSD-95 (Postsynaptic density protein of Mr 95kDa), Dlg (Drosophila Discs-Large protein) and ZO-1 (Zonula occludens protein 1) protein family.

17.   (previously presented) The method of claim 10, wherein the data accessed comprises data from the $p21^{ras}$ protein family.

18.   (previously presented) The method of claim 10, wherein the data accessed comprises data from the hemoglobin protein family.

19-35. (canceled)